EXHIBIT 6

DeCypher Results for Job: Smith-Waterman Similarity Search

Results by Query

Click on a query below to view its search results.

1394_PTH9903

Search Details

Results for: 1394_PTH9903; (Length=669/QuerySize=669)

Return to query summary

Maximum possible score for this scoring matrix and query: 6690.00

```
RANK    SCORES QF TARGET LOCUS NAME                    ACCESSION# TF TARGET
P_SCORE DESCRIPTION
1       3455.00  C gi|1787371|gb|AE000213.1|AE00021 AE000213.1  D
ecoli_ae  -1.0e+00 Escherichia coli K12 MG1655 section 103 of 400 of th
2        246.00  D gi|1787371|gb|AE000213.1|AE00021 AE000213.1  D
ecoli_ae  -1.0e+00 Escherichia coli K12 MG1655 section 103 of 400 of th
```

—

```
RANK 1 Score =  3455.00   P_Score =   -1.0e+00
 Q = CGI_3078ws206512.seq          QF =  C #Q Symbols = 669
 T = gi|1787371|gb|AE000213.1|AE00021 TF =  D #T Symbols = 10959
 A = AE000213.1
 D = Escherichia coli K12 MG1655 section 103 of 400 of the complete
genome
 Identical Match = 500  Similar = 500  Total # Of Gaps = 4
 Identity: Alignment = 75% Query = 74% Target = 4%
 Similarity: Alignment = 75% Query = 74% Target = 4%
 QS =     662  QE =        1  TS =     8606  TE =     9268

Q      662 TCCTT-AGGGGTAACATCCCGCCATTCCCCGTTTGCCAGCGAGTCCAGCGTATAGCTGCC
           TCCTT A   GT AC TC CGCCATTC CC TT GC AG    TCCA  G  TA      CC
T     8606 TCCTTAATCTGTCACTTCTCGCCATTCACCATTGGCAAGATTATCCAAAGAGTAATCACC

Q      603 CATGGCGTAGCGAATGAGTCGCAGGGTAGGGAAGCCCACATGCGCAGTCATGCGCCTGAC
```

```
          CAT GC TAGCGAAT AGTCGCAG GT GGGAAGCC ACATG GC GTCATGCG C  AC
T    8666 CATCGCATAGCGAATCAGTCGCAGCGTGGGGAAGCCAACATGGGCGGTCATGCGGCGCAC

Q     543 CTGTCGGTTGCGGCCTTCATAAAGGGTGATTTTAAGCCAGCTGGTAGGAATGGATTTACG
          CTG CG TT CG CCTTCATA A GGTGAT TT AGCCAGCTGGT GGAAT   TTT CG
T    8726 CTGGCGATTACGTCCTTCATATAAGGTGATCTTCAGCCAGCTGGTGGGAATACTTTTGCG

Q     483 CTCACGAATCGGCGGGTTGCGCGGCCACAGCCACTCGGGTTCATTCACACGTTCAATACC
          TCACGAAT GG GG TT CGCGGCCA A CCAC CGGGTTC T AC G TC   CC
T    8786 TTCACGAATTGGTGGATTCCGCGGCCATAACCACGCGGGTTCGTCAACCAGCTCCGCGCC

Q     423 AGCCGGCAGGGTGGGACCGTCGTTCAGCGTTACGCCGTTGCGCA--GCTTTGCCAGCGAC
          GC GGCAGGGT GG CC TC TT A GTTACGCC TTGCGCA GCTT   GCG C
T    8846 GGCGGGCAGGGTAGGGCCATCATTTAAGGTTACGCCATTGCGCAAGGCTTCAAGTGCGTC

Q     365 GCGTCGTCCGGCTCGCCTTCAACCTGCACATAGTAAATTTTTCCGGTACGTTTGCCCGGC
           GT GT  GG   CCTTC ACCTGCACATA TA ATTTTTCCGGT CGTTT CCCGGC
T    8906 TTGT-GT-GGGAATACCTTCCACCTGCACATAATAGATTTTTCCGGTGCGTTTACCCGGC

Q     305 TGAGTAAGCCTGGCCTGGAGCACGCCGTCATTGGTAAGGACCAGCAGCCCCTCGCTGTCG
          TG GT A  C  GCCTG A C CGCCGT ATTGGT AG ACCAGCA CCC TCGCT TCG
T    8964 TGGGTTAAACGCGCCTGCAACGCGCCGTTATTGGTCAGCACCAGCAACCCTTCGCTATCG

Q     245 CGATCCAGACGTCCCGCTGCGTAGACTCCCTGTACGGGGATAAAGTCCTTCAGCGTGCTG
          CG TC AG CG CC GCTGC TA AC CCCTG AC GGGAT AA TC TT A GT  TG
T    9024 CGGTCAAGGCGACCTGCTGCATAAACACCCTGAACCGGGATGAATTCTTTTAATGTTTTG

Q     185 CGCCCGGCCTCGTCGGTAAACTGCGGCAATACATCGTAGGGTTTATTGAACAGTATGACC
          CG CCGGC TC TCGGT AACTGCGG A  ACATCGTAGGGTTTATTGAACAG AT AC
T    9084 CGTCCGGCTTCATCGGTGAACTGCGGAAGAACATCGTAGGGTTTATTGAACAGGATCACA

Q     125 CGCGTTGGCTGGGGTTCTGGCGTTCTTCTGGTGGCTTGTCGTGAGCTGAATCGCTCAACC
          CGCGT GGCTGG  TTC GG  T C CTGGT G  GT G GAGCTGAATCGCT AACC
T    9144 CGCGTGGGCTGGTTTTCAGGTTTACGCCTGGTAGAACGTTGCGAGCTGAATCGCTTAACC

Q      65 CGGTGTTTTCTAAAAGAAGTTTTCGTCATGGTATTTTCAGGCGTTATCAATTGCCGCATT
          GGTG TTTCTAAAAGAAGTTTT   CATGGTATTTTCAG   TTAT AATTGCCGCATT
T    9204 TGGTGATTTCTAAAAGAAGTTTTTTGCATGGTATTTTCAGAGATTATGAATTGCCGCATT

Q       5 ATAGC
          ATAGC
T    9264 ATAGC
```

RANK 2 Score = 246.00 P_Score = -1.0e+00
Q = CGI_3078ws206512.seq   QF = D #Q Symbols = 669
T = gi|1787371|gb|AE000213.1|AE00021 TF = D #T Symbols = 10959
A = AE000213.1
D = Escherichia coli K12 MG1655 section 103 of 400 of the complete
genome
Identical Match = 197 Similar = 197 Total # Of Gaps = 22
Identity: Alignment = 52% Query = 29% Target = 1%
Similarity: Alignment = 52% Query = 29% Target = 1%
QS =   234 QE =   570 TS =   10054 TE =   10387

```
Q     234  ACGTCTGGATCGCGACAGCGAGGGGCTGCTGGTCCTTACCAATGACGGCGTGCTCCAGGC
           ACGTCTGG TCG G CAGCGA  G  T  C  G   TT C AA GA   CGTG   C G
T   10054  ACGTCTGGTTCGTG-CAGCGATCGAATAC--GCAATTGCTAACGA--TCGTGACTCTG--

Q     294  CAGGCTTACTCAGCCGGGCAAACGTACCGGAA--AAATTTAC--TATGTGCAGGTTGAAG
              T ACTC G  G  CAAA G A C   A  AA TT AC   A G GC G TT AAG
T   10107  -----TGACTCTGGTGCACAAAGGCAACATCATGAAGTTCACCGAAGGAGC-GTTTAAAG

Q     350  GCGAGCCGGACGACGCGTCGCTGGCAAAGCTGCGCAACGGCGTAACGCTGAACGACGGTC
              C G   AC A   G CGC  G A AG T  G   CGG G A   CTGA CGACGGT
T   10161  ACTGGGGCTACCAGCTGGCGCGTGAAGAGTTTGG---CGGTGAA---CTGATCGACGGTG

Q     410  CCACCCTGCCGGCTGGTATTGAACGTGTGAATGAACCCGAGTGGCTGTGGCCGCGCAACC
              C CC TG C            TGAA GT T AA  AACCCGA   C TGGC   G  A C
T   10215  GC-CCGTGGC---------TGAAAGT-TAAA--AACCCGA---ACACTGGCAAAGAGATC

Q     470  CGCCGATT------CGTGAGCGTAAATCCATTCCT--ACCAG-----------CTGGCTT
              C ATT      CGTGA G  AT CATTCCT  A CAG              C GGCT
T   10259  GTC--ATTAAAGACGTGATTGCTGATGCATTCCTGCAACAGATCCTGCTGCGTCCGGCTG

Q     511  AAAATCA-------CCCTTTATGAAGGCCGCAAC-----CGACAGGTCAGGCG-CATGAC
           AA AT A       CCT TATGAA  CC  AAC     C ACA  TC G CG C TG C
T   10317  AATATGATGTTATCGCCTGTATGAA--CCTGAACGGTGACTACATTTCTGACGCCCTGGC

Q     558  TGCGCATGTGGGC
           GCGCA GT GGC
T   10375  AGCGCAGGTTGGC
```

Job Details

[BEGIN JOB STATUS]

[BEGIN SEARCH TIME] Fri Dec 06 12:44:24 2002
[END SEARCH TIME] Fri Dec 06 12:44:24 2002
[VERSION] 7.3.0.27 G_SW_20
[SEARCH ID] CGI_3078ws206512.t10
[EOL] CRLF
[CGI INTERFACE VERSION] 2
[CGI JOB TITLE] Smith-Waterman Similarity Search
[COMMENT] /CGI_Ver=7.2.3.242
[ALGORITHM] SW
[MATRIX] d:\decypher\matrix/NUC4X4HB.MNT
[OPEN PENALTY] -20
[EXTEND PENALTY] -5
[FRAME PENALTY] 0
[QUERY FORMAT] FASTA/PEARSON
[QUERY TYPE] NT

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[QUERY SEARCH] D C
[QUERY PATH] d:\decypher\query
[QUERY SET] CGI_3078ws206512.seq
[TARGET TYPE] NT
[TARGET FRAMES] D
[TARGET PATH] d:\decypher\target
[OUTPUT FORMAT] COUNTDOWNCOMPLEMENT [USE SYSTEM] tblast-m
[TARGET SET] d:\decypher\target\ecoli_ae000213.txt
[SIGNIFICANCE] GAPPED
[MAX SCORES] 30
[MAX ALIGNMENTS] 20
[THRESHOLD] 1
[ALIGNMENT THRESHOLD] 20
[RESULT PATH] d:\decypher\output
[HTML RESULT PATH] C:\WebSite\cgi-temp\3078ws.out
[OUTPUT FORMAT] TEXT MAXSCORE PERCENTAGE EXTRACTALIGNED MATCHCHARACTER
[OUTPUT FORMAT] HTML WEB
[CGI REFERING PAGE] http://tblast-m.genomecorp.com/algo-sw/sw_nn.shtml
[CGI COOKIE] Set-Cookie: DeCypher=; expires=Saturday, 06-Dec-03
12:00:00 GMT; path=/; domain=tblast-m.genomecorp.com;


[JOB MESSAGES]


[END JOB STATUS]
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For assistance contact
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